
Sequence Listing was accepted.

See attached Validation Report.

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Reviewer: Durreshwar Anjum

Timestamp: Thu Oct 11 14:12:44 EDT 2007

Validated By CRFValidator v 1.0.3

Application No: 10756153 Version No: 2.0

Input Set:

Output Set:

Started: 2007-09-24 13:17:09.961 **Finished:** 2007-09-24 13:17:12.904

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 943 ms

Total Warnings: 16
Total Errors: 8

No. of SeqIDs Defined: 54

Actual SeqID Count: 54

Error code		Error Description
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (4)
W	213	Artificial or Unknown found in <213> in SEQ ID (10)
W	213	Artificial or Unknown found in <213> in SEQ ID (11)
W	213	Artificial or Unknown found in <213> in SEQ ID (12)
W	213	Artificial or Unknown found in <213> in SEQ ID (13)
W	213	Artificial or Unknown found in <213> in SEQ ID (14)
W	213	Artificial or Unknown found in <213> in SEQ ID (15)
W	213	Artificial or Unknown found in <213> in SEQ ID (16)
W	213	Artificial or Unknown found in <213> in SEQ ID (17)
W	213	Artificial or Unknown found in <213> in SEQ ID (18)
W	213	Artificial or Unknown found in <213> in SEQ ID (19)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (27)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (32)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (32)
W	213	Artificial or Unknown found in <213> in SEQ ID (44)
W	213	Artificial or Unknown found in <213> in SEQ ID (46)

Input Set:

Output Set:

Started: 2007-09-24 13:17:09.961 **Finished:** 2007-09-24 13:17:12.904

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 943 ms

Total Warnings: 16
Total Errors: 8
No. of SeqIDs Defined: 54

Actual SeqID Count: 54

Error code		Error Description									
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(50)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(51)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(52)
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SEQUENCE LISTING <110> Johnson, Leslie S. Li, Hua Tuaillon, Nadine <120> SOLUBLE FCgammaR FUSION PROTEINS AND METHODS OF USE THEREOF <130> 11183-005-999 <140> 10756153 <141> 2004-01-13 <141> 2004-01-13 <150> 60/439,709 <151> 2003-01-13 <160> 54 <170> FastSEQ version 4.0 <210> 1 <211> 420 <212> PRT <213> Homo sapiens <220> <223> sFcRIIIa-G2 <400> 1 Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln Gly 20 25 Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser 35 Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val

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65

55

70

Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser

75

80

Asp	Pro	Val	Gln	Leu 85	Glu	Val	His	Ile	Gly 90	Trp	Leu	Leu	Leu	Gln 95	Ala
Pro	Arg	Trp	Val 100	Phe	Lys	Glu	Glu	Asp 105	Pro	Ile	His	Leu	Arg 110	Суз	His
Ser	Trp	Lys 115	Asn	Thr	Ala	Leu	His 120	Lys	Val	Thr	Tyr	Leu 125	Gln	Asn	Gly
Lys	Gly 130	Arg	Lys	Tyr	Phe	His 135	His	Asn	Ser	Asp	Phe 140	Tyr	Ile	Pro	Lys
Ala 145	Thr	Leu	Lys	Asp	Ser 150	Gly	Ser	Tyr	Phe	Cys 155	Arg	Gly	Leu	Val	Gly 160
Ser	Lys	Asn	Val	Ser 165	Ser	Glu	Thr	Val	Asn 170	Ile	Thr	Ile	Thr	Gln 175	Gly
Leu	Ala	Val	Ser 180	Thr	Ile	Ser	Ser	Phe 185	Phe	Pro	Pro	Gly	Tyr 190	Gln	Val
Glu	Arg	Lys 195	Cys	Cys	Val	Glu	Cys 200	Pro	Pro	Cys	Pro	Ala 205	Pro	Pro	Val
Ala	Gly 210	Pro	Ser	Val	Phe	Leu 215	Phe	Pro	Pro	Lys	Pro 220	Lys	Asp	Thr	Leu
Met 225	Ile	Ser	Arg	Thr	Pro 230	Glu	Val	Thr	Суз	Val 235	Val	Val	Asp	Val	Ser 240
His	Glu	Asp	Pro	Glu 245	Val	Gln	Phe	Asn	Trp 250	Tyr	Val	Asp	Gly	Met 255	Glu
Val	His	Asn	Ala 260	Lys	Thr	Lys	Pro	Arg 265	Glu	Glu	Gln	Phe	Asn 270	Ser	Thr
Phe	Arg	Val 275	Val	Ser	Val	Leu	Thr 280	Val	Val	His	Gln	Asp 285	Trp	Leu	Asn
Gly	Lys 290	Glu	Tyr	Lys	Суз	Lys 295	Val	Ser	Asn	Lys	Gly 300	Leu	Pro	Ala	Pro
Ile 305	Glu	Lys	Thr	Ile	Ser 310	Lys	Thr	Lys	Gly	Gln 315	Pro	Arg	Glu	Pro	Gln 320
Val	Tyr	Thr	Leu	Pro 325	Pro	Ser	Arg	Glu	Glu 330	Met	Thr	Lys	Asn	Gln 335	Val
Ser	Leu	Thr	Cys 340	Leu	Val	Lys	Gly	Phe 345	Tyr	Pro	Ser	Asp	Ile 350	Ala	Val
Glu	Trp	Glu 355	Ser	Asn	Gly	Gln	Pro 360	Glu	Asn	Asn	Tyr	Lys 365	Thr	Thr	Pro

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr

370 375 380

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val 385 390 395 400

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu 405 410 415

Ser Pro Gly Lys 420

<210> 2

<211> 409

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIb-G2

<400> 2

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Ile Asn Val Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr 20 25 30

His Ser Pro Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu 35 40 45

Ile Pro Thr His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn
50 55 60

Asp Ser Gly Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp 65 70 75 80

Pro Val His Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro 85 90 95

His Leu Glu Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser $100 \,$ $105 \,$ $110 \,$

Trp Lys Asp Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys 115 120 125

Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala 130 135 140

Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro Ser

165 170 175

Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys 180 185 190

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys 195 200 205

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val 210 215 220

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr 225 230 235 240

Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu 245 250 255

Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His 260 265 270

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys 275 280 285

Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln 290 295 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met 305 310 315 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro 325 330 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn 340 345 350

Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu 355 360 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val 370 380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln 385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys 405

<210> 3

<211> 409

<212> PRT

<213> Homo sapiens

<400> 3

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Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro
20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr 35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly 50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu 85 90 95

Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp 100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys 115 120 125

Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser 130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe 145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser Met Gly Ser 165 170 175

Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys 180 185 190

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys 195 200 205

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val 210 215 220

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr 225 230 235 240

Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu 245 250 255

Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His 260 265 270

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

275 280 285

Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln 290 295 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met 305 310 315 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro 325 330 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn 340 345 350

Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu 355 360 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val 370 375 380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln 385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys 405

<210> 4

<211> 409

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIa(131H)-G2

<400> 4

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Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro 20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr 35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly 50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu

90 95

Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys Phe Ser His Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser Met Gly Ser Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln 290 295 300 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln 385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys 405

<210> 5

<211> 1382

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIB insert with signal sequence

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ggctcctgtt g	ctgggacac	ctgcagctcc	cccaaaggct	gtgctgaaac	tcgagcccca	180
gtggatcaac g	tgctccagg	aggactctgt	gactctgaca	tgccggggga	ctcacagccc	240
tgagagcgac t	ccattcagt	ggttccacaa	tgggaatctc	attcccaccc	acacgcagcc	300
cagctacagg t	tcaaggcca	acaacaatga	cagcggggag	tacacgtgcc	agactggcca	360
gaccagcctc a	gcgaccctg	tgcatctgac	tgtgctttct	gagtggctgg	tgctccagac	420
ccctcacctg ga	agttccagg	agggagaaac	catcgtgctg	aggtgccaca	gctggaagga	480
caageetetg g	tcaaggtca	cattcttcca	gaatggaaaa	tccaagaaat	tttcccgttc	540
ggatcccaac t	tctccatcc	cacaagcaaa	ccacagtcac	agtggtgatt	accactgcac	600
aggaaacata go	gctacacgc	tgttctcatc	caagcctgtg	accatcactg	tccaagctcc	660
cagctcttca c	ccatggagg	agcgcaaatg	ttgtgtcgag	tgcccaccgt	gcccagcacc	720
acctgtggca g	gaccgtcag	tcttcctttt	cccccaaaa	cccaaggaca	ccctcatgat	780
ctcccggacc c	ctgaggtca	cgtgcgtggt	ggtggacgtg	agccacgaag	accccgaggt	840
ccagttcaac to	ggtacgtgg	acggcatgga	ggtgcataat	gccaagacaa	agccacggga	900
ggagcagttc a	acagcacgt	tccgtgtggt	cagcgtcctc	accgtcgtgc	accaggactg	960
gctgaacggc a	aggagtaca	agtgcaaggt	ctccaacaaa	ggcctcccag	cccccatcga	1020

gaaaaccatc tccaaaacca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgccccc	1080
atcccgggag gagatgacca	agaaccaggt	cagcctgacc	tgcctggtca	aaggcttcta	1140
ccccagcgac atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	1200
cacacctccc atgctggact	ccgacggctc	cttcttcctc	tacagcaagc	tcaccgtgga	1260
caagagcagg tggcagcagg	ggaacgtctt	ctcatgctct	gtgatgcatg	aggctctgca	1320
caaccactac acacagaaga	gcctctccct	gtctccgggt	aaatgagtgc	ggccgcgaat	1380
tc					1382

<210> 6

<211> 1418

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIA insert

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cctcttcccc ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacgtg